

NEW SPECIES

“*Ruminococcus phoceensis*,” a new species identified from human stool from an obese patient before bariatric surgery

A. H. Togo¹, M. Maraninchi², F. Bittar¹, D. Raoult^{1,3} and M. Million¹

1) Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 2) Aix Marseille Université, NORT “Nutrition, Obesity and Risk of Thrombosis”, INSERM1062, INRA1260, Marseille, France and 3) Special Infectious Agents Unit, King Fahd Medical Research Center, King Abdulaziz University, Jeddah, Saudi Arabia

Abstract

We report here the main characteristics of a new bacterium species, “*Ruminococcus phoceensis*” strain AT10 (CSUR = P2086, DSM = 100837). This bacterium was isolated from the faeces of a 37-year-old woman from Marseille, France, with morbid obesity before bariatric surgery.

© 2016 The Authors. Published by Elsevier Ltd on behalf of European Society of Clinical Microbiology and Infectious Diseases.

Keywords: Bariatric surgery, culturomics, human gut microbiota, *Ruminococcus phoceensis*, taxonomy

Original Submission: 22 July 2016; **Revised Submission:** 5 August 2016; **Accepted:** 6 September 2016

Article published online: 10 September 2016

Corresponding author: M. Million, Aix-Marseille Université, URMITE, UM63, CNRS7278, IRD198, Inserm 1095, Institut Hospitalo-Universitaire Méditerranée-Infection, Faculté de médecine, 27 Boulevard Jean Moulin, 13385, Marseille Cedex 05, France
E-mail: matthieumillion@gmail.com

In July 2012, as a part of culturomics study [1] of the human microbiome, we isolated a new bacterial strain from the faeces of a 37-year-old woman from Marseille, France, with morbid obesity before she underwent bariatric surgery. Written consent was obtained from the patient at the nutrition, metabolic disease and endocrinology service of La Timone Hospital, Marseille, France. The study and the assent procedure were approved by the local ethics committee of IFR 48 under assent number 09-022, 2010.

Initial growth was obtained after 21 days of culture in a blood culture bottle (BACTEC Lytic/10 Anaerobic/F culture vials; Le Pont de Claix, Isère, France) enriched with 4 mL of sheep's blood and 4 mL of rumen under anaerobic atmosphere at 37°C. Agar-grown (Columbia agar + 5% sheep's blood; bioMérieux, Marcy l'Etoile, France) colonies were opalescent with a mean diameter of 0.5 to 1 mm. A bacterial strain could not be identified by our systematic matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) screening on Microflex spectrometer (Bruker Daltonics, Bremen, Germany) [2], so 16S rRNA gene sequencing was used for its identification.

Bacterial cells were Gram-positive staining, rod shaped and polymorphic, ranging 0.2–0.5 × 1.2–1.5 µm by electron microscopy. Strain AT10 was catalase positive and oxidase negative. The 16S rRNA gene was sequenced using fD1-rP2 primers as previously described with a 3130-XL sequencer (Applied Biosciences, Saint Aubin, France) [3]. Strain AT10 exhibited 98.2% of 16S rRNA gene sequence similarity with *Ruminococcus torques* ATCC 27756, the phylogenetically closest species with standing in nomenclature (Fig. 1), which putatively classifies it as a member of the genus *Ruminococcus* within the family *Ruminococcaceae* in the *Firmicutes* phylum. Strain AT10 exhibited a 16S rRNA gene sequence divergence of >1.3% (1.8) [4] with its phylogenetically closest species with standing in nomenclature, *Ruminococcus torques* [5].

We propose the creation of this new species, “*Ruminococcus phoceensis*” (pho.ce.en.sis, N.L. gen. n. *phoceensis*, based on the acronym of the Phoecean city where the type strain was isolated). Strain AT10 is the type strain of the new species “*Ruminococcus phoceensis*.”

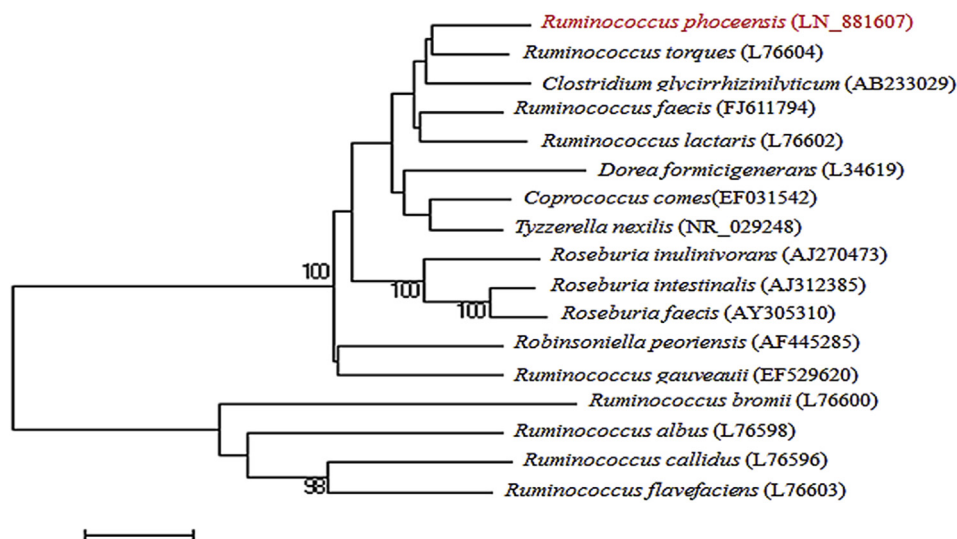


FIG. 1. Phylogenetic tree showing position of strain AT10 relative to other phylogenetically close neighbours. Sequences were aligned using CLUSTALW, and phylogenetic inferences were obtained using maximum-likelihood method within MEGA software. Numbers at nodes are percentages of bootstrap values obtained by repeating analysis 500 times to generate majority consensus tree. Only bootstraps scores of at least 90% were retained. Scale bar indicates 2% nucleotide sequence divergence.

MALDI-TOF MS spectrum accession number

The MALDI-TOF MS spectrum of this strain is available online (<http://mediterranean-infection.com/article.php?laref=256&titre=urms-database>).

Nucleotide sequence accession number

The 16S rRNA gene sequence was deposited in GenBank under accession number LN881607.

Deposit in a culture collection

Strain AT10 was deposited in the Collection de Souches de l'Unité des Rickettsies and Deutsche Sammlung von Mikroorganismen (CSUR = P2086, DSM = 100837).

Acknowledgements

The authors thank M. Lardière for English-language review. This study was funded by the Fondation Méditerranée Infection.

Conflict of Interest

None declared.

References

- [1] Lagier JC, Armougom F, Million M, Hugon P, Pagnier I, Robert C, et al. Microbial culturomics: paradigm shift in the human gut microbiome study. *Clin Microbiol Infect* 2012;18:1185–93.
- [2] Seng P, Drancourt M, Gouriet F, La Scola B, Fournier PE, Rolain JM, et al. Ongoing revolution in bacteriology: routine identification of bacteria by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. *Clin Infect Dis* 2009;49:543–51.
- [3] Drancourt M, Bollet C, Carlioz A, Martelin R, Gayral JP, Raoult D. 16S ribosomal DNA sequence analysis of a large collection of environmental and clinical unidentifiable bacterial isolates. *J Clin Microbiol* 2000;38:3623–30.
- [4] Stackebrandt E, Ebers J. Taxonomic parameters revisited: tarnished gold standards. *Microbiol Today* 2006;33:152–5.
- [5] Huson DH, Richter DC, Rausch C, Dezulian T, Franz M, Rupp R. Dendroscope: an interactive viewer for large phylogenetic trees. *BMC Bioinformatics* 2007;8:460.